AMENDMENTS TO THE SPECIFICATION

At page 8, please replace the paragraph starting from line 1 with the following rewritten paragraph:

Table 2 shows numbers from 1 to 259 imparted to 259 genes in association with systematic gene names thereof. These systematic gene names correspond to the names registered as systematic names in yeast genome database (*Saccharomyces cerevisiae* genome database~~; http://genome-www.stanford.edu/Saccharomyces/~~.) Accordingly, the genes of *Saccharomyces cerevisiae* described in the above Table 2 can easily be specified by using such a systematic gene name as a key and searching for the systematic name through the yeast genome database. Moreover, the nucleotide sequences of the genes of *Saccharomyces cerevisiae* described in Table 2 can be obtained by searching through the yeast genome database. Furthermore, other types of information regarding the genes of *Saccharomyces cerevisiae* described in Table 2 can also be obtained by searching through the yeast genome database.

At page 30, please replace the first paragraph under the table with the following rewritten paragraph:

Table 4 shows: systematic gene names of yeasts; common names (only in a case where such a common name is given) (wherein, with regard to these gene names and common names, please refer to the yeast genome database (*Saccharomyces cerevisiae* genome database; ~~http://genome-www.stanford.edu/Saccharomyces/~~); and the ratios of the normalized values of fluorescence intensities of post-low temperature treatment samples at various periods of time to the normalized values of fluorescence intensities of post-low temperature treatment samples at various periods of time to the normalized values of fluorescence intensities of pre-low temperature treatment samples.

Please replace the paragraph bridging pages 31 and 32 with the following rewritten paragraph:

Subsequently, the prepared HSP12 fragment was ligated to a pT7Blue T-vector (Novagen), and Escherichia coli DH5α was transformed with the obtained vector. Several transformants were cultured in a test tube, and a plasmid was then prepared using Quantum Prep Plasmid MiniPrep kit (Bio-Rad). Based on a cleavage pattern made by restriction enzymes, a transformant containing a plasmid of interest was identified. Thereafter, the obtained transformant was cultured in 80 ml of a culture solution, and a plasmid was prepared using QuantumPrep Plasmid MidiPrep kit (Bio-Rad). The nucleotide sequence of the obtained HSP12 fragment was sequence using DNA sequencing kit (Applied Biosystems), and the obtained nucleotide sequence of the HSP12 fragment was compared with the nucleotide sequence of HSP12 in the genome database (*Saccharomyces cerevisiae* genome database~~; http://genome-www.stanford.edu/Saccharomyces/~~), so as to identify it. Thereafter, an HSP12 fragment was cut out of the pT7Blue T-vector containing the HSP12 fragment, using restriction enzymes. The HSP12 fragment was then separated and recovered by agarose gel electrophoresis using low melting point agarose (FMC). The thus obtained HSP12 fragment was labeled with alkaline phosphatase, using AlkPhos Direct Labeling Module (Amersham Biotech) in accordance with the protocol attached therewith.

At page 35, please replace the paragraph starting from line 1 with the following rewritten paragraph:

Subsequently, the isolated DNA was inserted into the site located upstream of the ORF of an enhanced green fluorescent protein (EGFP) in a reporter plasmid pUG35-MET25. It is to be noted that the pUG35-MET25 plasmid was produced by cleaving pUG35 ~~(http://www.mips.biochem.mpg.de/proj/yeast/info/tools/index.html)~~ with *Xba*I and *Sac*I, and blunt-ending the cleaved portion with T4 DNA polymerase, followed by the self-cyclization of the obtained product. The pUG35-MET25 plasmid was cleaved with *Sal*I, and then converted into a blunt end with T4 DNA polymerase. Thereafter, hydroxyl groups at both ends of the DNA fragment having a DBP2 cold-inducible promoter function, which had been isolated by PCR, were phosphorylated with T4 DNA kinase and ATP. The phosphorylated

DNA fragment having a DBP2 promoter function was ligated to the blunt-ended pUG35-MET25 plasmid, using TaKaRa DNA Ligation Kit ver. 2 in accordance with the protocol attached with the kit. Thereafter, *Escherichia coli* DH5α was transformed with the ligated product. Several transformants as obtained above were cultured in 3 ml of a culture solution overnight, and plasmids were then prepared using QuantumPrep Plasmid MiniPrep kit. Based on a cleavage pattern made by restriction enzymes, a transformant containing a plasmid of interest was identified. In addition, at this time, a plasmid in which a DBP2 promoter is adjacent upstream of EGFP ORF (forward direction; Figure 8), and a plasmid in which a region adjacent to an RPC19 side is ligated immediately upstream of EGFP ORF (reverse direction), were isolated. Thereafter, a transformant obtained in each case was cultured in 80 ml of a culture solution, and a plasmid was then prepared using QuantumPrep Plasmid MidiPrep kit. A yeast strain *Saccharomyces cerevisiae* YPH500 was transformed with this plasmid. Transformation was carried out by the method described in Yeast Protocol Handbook published from Invitrogen. The obtained transformed yeast was cultured at 30°C, and at the time when the absorbance at 600 nm became 1, sampling was carried out at 0 minute. Thereafter, the culture temperature was decreased from 30°C to 10°C, and the culture was continuously carried out. Then, sampling was carried out in the same manner as described above.